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<120> Regulation of Angiogenesis With Zinc  
Finger Proteins

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<151> 2000-12-07

<150> US 09/736,083  
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Arg Ser Asp Ala Leu Thr Gln

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Arg Ser Asp His Leu Ser Arg

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<220>

<223> finger

<400> 171

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<210> 172

<211> 7

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Arg Ser Asp His Leu Ser Arg

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<220>

<223> finger

<400> 173

Arg Ser Asp Asn Leu Ala Arg

1

5

<210> 174

<211> 7

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&lt;223&gt; finger

&lt;400&gt; 174

Arg Ser Asp His Leu Ser Arg  
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&lt;210&gt; 175

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 175

Arg Ser Asp Asn Leu Thr Gln  
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&lt;210&gt; 176

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 176

Asp Arg Ser Ser Leu Thr Arg  
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&lt;210&gt; 177

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 177

Arg Ser Asp His Leu Ser Arg  
1 5

&lt;210&gt; 178

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; finger

&lt;400&gt; 178

Gln Ser Gly Ser Leu Thr Arg  
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&lt;210&gt; 179

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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<221> modified\_base

<222> (26)...(26)

<223> n = a modified by tetramethylrhodamine (TAMRA)

<400> 206

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26

<210> 207

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> target

<400> 207

tgagcggcgg cagcggagc

19

<210> 208

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

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class of zinc finger proteins (ZFP)

<221> MOD\_RES

<222> (2)...(5)

<223> Xaa = any amino acid, Xaa in positions 4 and 5 may  
be present or absent

<221> MOD\_RES

<222> (7)...(18)

<223> Xaa = any amino acid

<221> MOD\_RES

<222> (20)...(24)

<223> Xaa = any amino acid, Xaa in positions 23 and 24  
may be present or absent

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 1 5 10 15  
 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His  
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<210> 209  
 <211> 9  
 <212> DNA  
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<220>  
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<400> 209  
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9

<210> 210  
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 <212> DNA  
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<220>  
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<400> 210  
 ggcgacgta

9

<210> 211  
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<210> 212  
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<220>  
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<400> 212  
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Gly Gly Arg Arg Gly Gly Gly Ser  
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<400> 214

Leu Arg Gln Arg Asp Gly Glu Arg Pro  
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<400> 216

Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro  
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<210> 217  
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<220>  
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factor Zif268

<400> 217

Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp  
1 5 10 15  
Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro  
20 25 30

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## factor Zif268

<400> 218  
 Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu  
 1 5 10 15  
 Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro  
 20 25

<210> 219  
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 factor Zif268

<400> 219  
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 1 5 10 15  
 Lys Arg His Thr Lys Ile His Leu Arg Gln Lys  
 20 25

<210> 220  
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<220>  
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<400> 220  
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 <211> 94  
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 Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp His Thr  
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 35 40 45  
 Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr Gly Glu  
 50 55 60  
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 65 70 75 80  
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 85 90

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&lt;223&gt; Sp-1 optimal target consensus sequence

&lt;400&gt; 222

ggggcgggg

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&lt;210&gt; 223

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Sp-i consensus sequence with leader sequence

&lt;400&gt; 223

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1				5				10					15		
His	Ala	Cys	Pro	Glu	Cys	Gly	Lys	Ser	Phe	Ser	Lys	Ser	Ser	His	Leu
			20					25					30		
Arg	Ala	His	Gln	Arg	Thr	His	Thr	Gly	Glu	Arg	Pro	Tyr	Lys	Cys	Pro
		35					40					45			
Glu	Cys	Gly	Lys	Ser	Phe	Ser	Arg	Ser	Asp	Glu	Leu	Gln	Arg	His	Gln
	50					55				60					
Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Pro	Glu	Cys	Gly	Lys
65					70				75					80	
Ser	Phe	Ser	Arg	Ser	Asp	His	Leu	Ser	Lys	His	Gln	Arg	Thr	His	Gln
				85					90					95	
Asn	Lys	Lys	Gly												
			100												

&lt;210&gt; 224

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; N-terminal nuclear localization signal from SV40 large T antigen

&lt;400&gt; 224

Pro	Lys	Lys	Lys	Arg	Lys	Val
1				5		

&lt;210&gt; 225

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; FLAG peptide

&lt;400&gt; 225

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
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&lt;210&gt; 226

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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 <400> 227  
 actcgatctc atcagggtac tc 22  
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 <222> (1)...(1)  
 <223> n = c modified by aminofluorescein (FAM)  


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 <222> (25)...(25)  
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 <400> 228  
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 <400> 230  
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<220>
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<221> modified_base
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<221> modified_base
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<400> 231
ncctgcacca ccaactgctt agcn                                     24

<210> 232
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<220>
<223> VP16-FLAG forward primer

<400> 232
catgacgatt tcgatctgga                                         20

<210> 233
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<220>
<223> VP16-FLAG reverse primer

<400> 233
ctacttgatca tcgtcgtcct tg                                     22

<210> 234
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<220>
<223> VP16-FLAG Taqman probe

<221> modified_base
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<221> modified_base
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<400> 234
ntcggtaaac atctgctcaa actcgn                                     26

<210> 235
<211> 28
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<220>  
 <223> RT-PCR primer  
  
 <400> 235  
 atgaactttc tgctgtcttg ggtgcatt 28  
  
 <210> 236  
 <211> 22  
 <212> DNA  
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 <223> RT-PCR primer  
  
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 tcaccgcctc ggcttgtcac at 22  
  
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 <211> 18  
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 <400> 237  
 tgagcggcgg cagcggag 18

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<210> 238  
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 Arg Ser Asp Glu Leu Ser Arg  
 1 5  
  
 <210> 239  
 <211> 7  
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 <400> 239  
 Gln Ser Gly His Leu Thr Lys  
 1 5  
  
 <210> 240  
 <211> 10  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> target  
  
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gctgggggag

10

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<220>  
 <223> primer

<400> 241  
 cccagatctg gtgatggcaa gaagaagcag caccatctgc cacatccag

49

<210> 242  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 242  
 cccaagctta ggatccaccc ttcttgttct ggtgggt

37

<210> 243  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VZ+57

<400> 243  
 His Gln Asn Lys Lys Gly Gly Ser Gly Asp Gly Lys Lys Lys Gln His  
 1 5 10 15  
 Ile Cys

<210> 244  
 <211> 9  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> target

<400> 244  
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9

<210> 245  
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<220>  
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<400> 245  
 Thr Ser Gly His Leu Thr Arg  
 1 5

<210> 246  
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<220>  
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<400> 246  
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<210> 247  
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<220>  
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<400> 247  
 Thr Ser Gly His Leu Ser Arg  
 1 5

<210> 248  
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<220>  
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<400> 248  
 Thr Ser Gly His Leu Ala Arg  
 1 5

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<220>  
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<400> 249  
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<210> 250  
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<220>  
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<400> 250  
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 1 5

<210> 251  
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<212> PRT  
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<220>  
<223> finger

<400> 251  
Thr Thr Gly His Leu Val Arg  
1 5

<210> 252  
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<212> PRT  
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<220>  
<223> finger

<400> 252  
Thr Lys Asp His Leu Val Arg  
1 5

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